



## SEQUENCE LISTING

<110> Caput, Daniel  
Ferrara, Pascual  
Laurent, Patrick  
Vita, Natalio

<120> IL-13 RECEPTOR

<130> IVD924

<140> 09/077,817

<141> 1998-09-14

<150> PCT/FR96/01756

<151> 1996-11-07

<160> 15

<170> PatentIn Ver. 2.0

<210> 1

<211> 1539

<212> DNA

<213> Homo sapiens

<400> 1

GGTGCCTGTC GGCAGGGGAGA GAGGCAATAT CAAGGTTTTA AATCTCGGAG AAATGGCTTT 60  
CGTTTGCTTG GCTATCGGAT GCTTATATAC CTTTCTGATA AGCACAACAT TTGGCTGTAC 120  
TTCATCTTCA GACACCGAGA TAAAAGTTAA CCCTCCTCAG GATTTTGAGA TAGTGGATCC 180  
CGGATACTTA GGTTATCTCT ATTTGCAATG GCAACCCCCA CTGTCTCTGG ATCATTTTAA 240  
GGAATGCACA GTGGAATATG AACTAAAATA CCGAAACATT GGTAGTGAAA CATGGAAGAC 300  
CATCATTACT AAGAATCTAC ATTACAAAGA TGGGTTTGAT CTTAACAAGG GCATTGAAGC 360  
GAAGATACAC ACGCTTTTAC CATGGCAATG CACAAATGGA TCAGAAGTTC AAAGTTCCTG 420  
GGCAGAAACT ACTTATTGGA TATCACCACA AGGAATTCCA GAAACTAAAG TTCAGGATAT 480  
GGATTGCGTA TATTACAATT GGCAATATTT ACTCTGTTCT TGGAAACCTG GCATAGGTGT 540  
ACTTCTTGAT ACCAATTACA ACTTGTTTTA CTGGTATGAG GGCTTGGATC ATGCATTACA 600  
GTGTGTTGAT TACATCAAGG CTGATGGACA AAATATAGGA TGCAGATTTC CCTATTTGGA 660  
GGCATCAGAC TATAAAGATT TCTATATTTG TGTTAATGGA TCATCAGAGA ACAAGCCTAT 720  
CAGATCCAGT TATTTCACTT TTCAGCTTCA AAATATAGTT AAACCTTTGC CGCCAGTCTA 780  
TCTTACTTTT ACTCGGGAGA GTTCATGTGA AATTAAGCTG AAATGGAGCA TACCTTTGGG 840  
ACCTATTCCA GCAAGGTGTT TTGATTATGA AATTGAGATC AGAGAAGATG ATACTACCTT 900  
GGTGACTGCT ACAGTTGAAA ATGAAACATA CACCTTGAAA ACAACAAATG AAACCCGACA 960  
ATTATGCTTT GTAGTAAGAA GCAAAGTGAA TATTTATTGC TCAGATGACG GAATTTGGAG 1020

TGAGTGGAGT GATAACAAT GCTGGGAAGG TGAAGACCTA TCGAAGAAAA CTTTGCTACG 1080  
 TTTCTGGCTA CCATTGGTT TCATCTTAAT ATTAGTTATA TTTGTAACCG GTCTGCTTTT 1140  
 GCGTAAGCCA AACACCTACC CAAAAATGAT TCCAGAATTT TTCTGTGATA CATGAAGACT 1200  
 TTCCATATCA AGAGACATGG TATTGACTCA ACAGTTTCCA GTCATGGCCA AATGTTCAAT 1260  
 ATGAGTCTCA ATAAACTGAA TTTTCTTGC GAATGTTG 1298

<210> 2  
 <211> 380  
 <212> PRT  
 <213> Homo sapiens

<400> 2

Met Ala Phe Val Cys Leu Ala Ile Gly Cys Leu Tyr Thr Phe Leu Ile  
 1 5 10 15  
 Ser Thr Thr Phe Gly Cys Thr Ser Ser Asp Thr Glu Ile Lys Val  
 20 25 30  
 Asn Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr  
 35 40 45  
 Leu Tyr Leu Gln Trp Gln Pro Pro Leu Ser Leu Asp His Phe Lys Glu  
 50 55 60  
 Cys Thr Val Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Gly Ser Glu Thr  
 65 70 75 80  
 Trp Lys Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp  
 85 90 95  
 Leu Asn Lys Gly Ile Glu Ala Lys Ile His Thr Leu Leu Pro Trp Gln  
 100 105 110  
 Cys Thr Asn Gly Ser Glu Val Gln Ser Ser Trp Ala Glu Thr Thr Tyr  
 115 120 125  
 Trp Ile Ser Pro Gln Gly Ile Pro Glu Thr Lys Val Gln Asp Met Asp  
 130 135 140  
 Cys Val Tyr Tyr Asn Trp Gln Tyr Leu Leu Cys Ser Trp Lys Pro Gly  
 145 150 155 160  
 Ile Gly Val Leu Leu Asp Thr Asn Tyr Asn Leu Phe Tyr Trp Tyr Glu  
 165 170 175  
 Gly Leu Asp His Ala Leu Gln Cys Val Asp Tyr Ile Lys Ala Asp Gly  
 180 185 190  
 Gln Asn Ile Gly Cys Arg Phe Pro Tyr Leu Glu Ala Ser Asp Tyr Lys  
 195 200 205  
 Asp Phe Tyr Ile Cys Val Asn Gly Ser Ser Glu Asn Lys Pro Ile Arg  
 210 215 220  
 Ser Ser Tyr Phe Thr Phe Gln Leu Gln Asn Ile Val Lys Pro Leu Pro  
 225 230 235 240  
 Pro Val Tyr Leu Thr Phe Thr Arg Glu Ser Ser Cys Glu Ile Lys Leu  
 245 250 255  
 Lys Trp Ser Ile Pro Leu Gly Pro Ile Pro Ala Arg Cys Phe Asp Tyr  
 260 265 270  
 Glu Ile Glu Ile Arg Glu Asp Asp Thr Thr Leu Val Thr Ala Thr Val  
 275 280 285  
 Glu Asn Glu Thr Tyr Thr Leu Lys Thr Thr Asn Glu Thr Arg Gln Leu  
 290 295 300  
 Cys Phe Val Val Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly  
 305 310 315 320  
 Ile Trp Ser Glu Trp Ser Asp Lys Gln Cys Trp Glu Gly Glu Asp Leu

3  
 Cont

				325						330					335				
Ser	Lys	Lys	Thr	Leu	Leu	Arg	Phe	Trp	Leu	Pro	Phe	Gly	Phe	Ile	Leu				
			340						345				350						
Ile	Leu	Val	Ile	Phe	Val	Thr	Gly	Leu	Leu	Leu	Arg	Lys	Pro	Asn	Thr				
		355					360					365							
Tyr	Pro	Lys	Met	Ile	Pro	Glu	Phe	Phe	Cys	Asp	Thr								
	370					375					380								

&lt;210&gt; 3

&lt;211&gt; 4009

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3

TCAGCCCGGC	CGGGCTCCGA	GGCGAGAGGC	TGCATGGAGT	GGCCGGCGCG	GCTCTGCGGG	60
CTGTGGGCGC	TGCTGCTCTG	CGCCGGCGGC	GGGGGCGGGG	GCGGGGCGCG	CGCGCCTACG	120
GAAACTCAGC	CACCTGTGAC	AAATTTGAGT	GTCTCTGTTG	AAAACCTCTG	CACAGTAATA	180
TGGACATGGA	ATCCACCCGA	GGGAGCCAGC	TCAAATTGTA	GTCTATGGTA	TTTtagTCAT	240
TTTGGCGACA	AACAAGATAA	GAAAATAGCT	CCGGAAACTC	GTCGTTCAAT	AGAAGTACCC	300
CTGAATGAGA	GGATTTGTCT	GCAAGTGGGG	TCCCAGTGTA	GCACCAATGA	GAGTGAGAAG	360
CCTAGCATTT	TGGTTGAAAA	ATGCATCTCA	CCCCCAGAAG	GTGATCCTGA	GTCTGCTGTG	420
ACTGAGCTTC	AATGCATTTG	GCACAACCTG	AGCTACATGA	AGTGTTCTTG	GCTCCCTGGA	480
AGGAATACCA	GTCCCGACAC	TAActATACT	CTCTACTATT	GGCACAGAAG	CCTGGAAAAA	540
ATTCATCAAT	GTGAAAACAT	CTTTAGAGAA	GGCCAATACT	TTGGTTGTTC	CTTTGATCTG	600
ACCAAAGTGA	AGGATTCCAG	TTTTGAACAA	CACAGTGTCC	AAATAATGGT	CAAGGATAAT	660
GCAGGAAAAA	TTAAACCATC	CTTCAATATA	GTGCCTTTAA	CTTCCCGTGT	GAAACCTGAT	720
CCTCCACATA	TTAAAAACCT	CTCCTTCCAC	AATGATGACC	TATATGTGCA	ATGGGAGAAT	780
CCACAGAATT	TTATTAGCAG	ATGCCTATTT	TATGAAGTAG	AAGTCAATAA	CAGCCAAACT	840
GAGACACATA	ATGTTTTCTA	CGTCCAAGAG	GCTAAATGTG	AGAATCCAGA	ATTTGAGAGA	900
AATGTGGAGA	ATACATCTTG	TTTCATGGTC	CCTGGTGTTT	TTCCTGATAC	TTTGAACACA	960
GTCAGAATAA	GAGTCAAAAC	AAATAAGTTA	TGCTATGAGG	ATGACAAACT	CTGGAGTAAT	1020
TGGAGCCAAG	AAATGAGTAT	AGGTAAGAAG	CGCAATTCCA	CACTCTACAT	AACCATGTTA	1080
CTCATTGTTC	CAGTCATCGT	CGCAGGTGCA	ATCATAGTAC	TCCTGCTTTA	CCTAAAAAGG	1140
CTCAAGATTA	TTATATTCCC	TCCAATTCCCT	GATCCTGGCA	AGATTTTTTAA	AGAAATGTTT	1200
GGAGACCAGA	ATGATGATAC	TCTGCACTGG	AAGAAGTACG	ACATCTATGA	GAAGCAAACC	1260
AAGGAGGAAA	CCGACTCTGT	AGTGCTGATA	GAAAACCTGA	AGAAAGCCTC	TCAGTGATGG	1320
AGATAATTTA	TTTTTACCTT	CACTGTGACC	TTGAGAAGAT	TCTTCCCAT	CTCCATTTGT	1380

1  
Cont

TATCTGGGAA CTTATTAAAT GGAAACTGAA ACTACTGCAC CATTAAAAA CAGGCAGCTC 1440  
 ATAAGAGCCA CAGGTCTTTA TGTGAGTCG CGCACCGAAA AACTAAAAAT AATGGGCGCT 1500  
 TTGGAGAAGA GTGTGGAGTC ATTCTCATTG AATTATAAAA GCCAGCAGGC TTCAAAC TAG 1560  
 GGGACAAAGC AAAAAGTGAT GATAGTGGTG GAGTTAATCT TATCAAGAGT TGTGACAACT 1620  
 TCCTGAGGGA TCTATACTTG CTTTGTGTTC TTTGTGTCAA CATGAACAAA TTTTATTTGT 1680  
 AGGGGAACTC ATTTGGGGTG CAAATGCTAA TGTCAAACCTT GAGTCACAAA GAACATGTAG 1740  
 AAAACAAAAT GGATAAAATC TGATATGTAT TGTTTGGGAT CCTATTGAAC CATGTTTGTG 1800  
 GCTATTAAAA CTCTTTTAAC AGTCTGGGCT GGGTCCGGTG GCTCACGCCT GTAATCCCAG 1860  
 CAATTTGGGA GTCCGAGGCG GGCGGATCAC TCGAGGTCAG GAGTTCCAGA CCAGCCTGAC 1920  
 CAAAATGGTG AAACCTCCTC TCTACTAAAA CTACAAAAAT TAACTGGGTG TGGTGGCGCG 1980  
 TGCCTGTAAT CCCAGCTACT CGGGAAGCTG AGGCAGGTGA ATTGTTTGAA CTGGGAGGT 2040  
 GGAGGTTGCA GTGAGCAGAG ATCACACCAC TGCACTCTAG CCTGGGTGAC AGAGCAAGAC 2100  
 TCTGTCTAAA AAACAAAACA AAACAAAACA AAACAAAAAA ACCTCTTAAT ATTCTGGAGT 2160  
 CATCATCCC TTCGACAGCA TTTTCCTCTG CTTTGAAAGC CCCAGAAATC AGTGTGGGCC 2220  
 ATGATGACAA CTACAGAAAA ACCAGAGGCA GCTTCTTTGC CAAGACCTTT CAAAGCCATT 2280  
 TTAGGCTGTT AGGGGCAGTG GAGGTAGAAT GACTCCTTGG GTATTAGAGT TTCAACCATG 2340  
 AAGTCTCTAA CAATGTATTT TCTTCACCTC TGCTACTCAA GTAGCATTTA CTGTGTCTTT 2400  
 GGTTTGTGCT AGGCCCCCGG GTGTGAAGCA CAGACCCCTT CCAGGGGTTT ACAGTCTATT 2460  
 TGAGACTCCT CAGTTCTTGC CACTTTTTTT TTTAATCTCC ACCAGTCATT TTTAGACCT 2520  
 TTTAACTCCT CAATTCCAAC ACTGATTTC CTTTTGCAT TCTCCCTCCT TCCCTTCCTT 2580  
 GTAGCCTTTT GACTTTTATT GGAAATTAGG ATGTAAATCT GCTCAGGAGA CCTGGAGGAG 2640  
 CAGAGGATAA TTAGCATCTC AGGTAAAGTG TGAGTAATCT GAGAAACAAT GACTAATTCT 2700  
 TGCATATTTT GTAACCTCCA TGTGAGGGTT TTCAGCATTG ATATTGTGC ATTTTCTAAA 2760  
 CAGAGATGAG GTGGTATCTT CACGTAGAAC ATTGGTATTC GCTTGAGAAA AAAAGAATAG 2820  
 TTGAACCTAT TTCTCTTTCT TTACAAGATG GGTCCAGGAT TCCTCTTTTC TCTGCCATAA 2880  
 ATGATTAATT AAATAGCTTT TGTGTCTTAC ATTGGTAGCC AGCCAGCCAA GGCTCTGTTT 2940  
 ATGCTTTTGG GGGGCATATA TTGGGTCCA TTCTCACCTA TCCACACAAC ATATCCGTAT 3000  
 ATATCCCCTC TACTCTTACT TCCCCAAAT TTAAAGAAGT ATGGGAAATG AGAGGCATTT 3060  
 CCCCCACCC ATTTCTCTCC TCACACACAG ACTCATATTA CTGGTAGGAA CTTGAGAACT 3120  
 TTATTTCCAA GTTGTTCAAA CATTTACCAA TCATATTAAT ACAATGATGC TATTTGCAAT 3180

31  
 Cont.

TCCTGCTCCT AGGGGAGGGG AGATAAGAAA CCCTCACTCT CTACAGGTTT GGGTACAAGT 3240  
 GGCAACCTGC TTCCATGGCC GTGTAGAAGC ATGGTGCCCT GGCTTCTCTG AGGAAGCTGG 3300  
 GGTTCATGAC AATGGCAGAT GTAAAGTTAT TCTTGAAGTC AGATTGAGGC TGGGAGACAG 3360  
 CCGTAGTAGA TGTCTACTT TGTCTGCTG TTCTCTAGAA AGAATATTG GTTTCTCTGT 3420  
 ATAGGAATGA GATTAATTCC TTTCCAGGTA TTTTATAATT CTGGGAAGCA AAACCCATGC 3480  
 CTCCCCCTAG CCATTTTAC TGTATCCTA TTTAGATGGC CATGAAGAGG ATGCTGTGAA 3540  
 ATTCCCAACA AACATTGATG CTGACAGTCA TGCAGTCTGG GAGTGGGGAA GTGATCTTTT 3600  
 GTTCCCATCC TCTTCTTTTA GCAGTAAAT AGCTGAGGGA AAAGGGAGGG AAAAGGAAGT 3660  
 TATGGGAATA CCTGTGGTGG TTGTGATCCC TAGGTCTTGG GAGCTCTTGG AGGTGTCTGT 3720  
 ATCAGTGGAT TTCCCATCCC CTGTGGGAAA TTAGTAGGCT CATTTACTGT TTTAGGTCTA 3780  
 GCCTATGTGG ATTTTTTCCT AACATACCTA AGCAAACCCA GTGTCAGGAT GGTAATTCTT 3840  
 ATTCTTTCGT TCAGTTAAGT TTTCCCTTC ATCTGGGCAC TGAAGGGATA TGTGAAACAA 3900  
 TGTTAACATT TTTGGTAGTC TTCAACCAGG GATTGTTTCT GTTTAACTTC TTATAGGAAA 3960  
 GCTTGAGTAA AATAAATATT GTCTTTTGT ATGTCACCCA AAAAAAAAAA 4009

<210> 4  
 <211> 427  
 <212> PRT  
 <213> Homo sapiens

<400> 4

Met Glu Trp Pro Ala Arg Leu Cys Gly Leu Trp Ala Leu Leu Leu Cys  
 1 5 10 15  
 Ala Gly Gly Gly Gly Gly Gly Gly Gly Ala Ala Pro Thr Glu Thr Gln  
 20 25 30  
 Pro Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Val  
 35 40 45  
 Ile Trp Thr Trp Asn Pro Pro Glu Gly Ala Ser Ser Asn Cys Ser Leu  
 50 55 60  
 Trp Tyr Phe Ser His Phe Gly Asp Lys Gln Asp Lys Lys Ile Ala Pro  
 65 70 75 80  
 Glu Thr Arg Arg Ser Ile Glu Val Pro Leu Asn Glu Arg Ile Cys Leu  
 85 90 95  
 Gln Val Gly Ser Gln Cys Ser Thr Asn Glu Ser Glu Lys Pro Ser Ile  
 100 105 110  
 Leu Val Glu Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala  
 115 120 125  
 Val Thr Glu Leu Gln Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys  
 130 135 140  
 Ser Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr Asn Tyr Thr Leu  
 145 150 155 160  
 Tyr Tyr Trp His Arg Ser Leu Glu Lys Ile His Gln Cys Glu Asn Ile  
 165 170 175  
 Phe Arg Glu Gly Gln Tyr Phe Gly Cys Ser Phe Asp Leu Thr Lys Val  
 180 185 190

1  
 Cons

Lys Asp Ser Ser Phe Glu Gln His Ser Val Gln Ile Met Val Lys Asp  
 195 200 205  
 Asn Ala Gly Lys Ile Lys Pro Ser Phe Asn Ile Val Pro Leu Thr Ser  
 210 215 220  
 Arg Val Lys Pro Asp Pro Pro His Ile Lys Asn Leu Ser Phe His Asn  
 225 230 235 240  
 Asp Asp Leu Tyr Val Gln Trp Glu Asn Pro Gln Asn Phe Ile Ser Arg  
 245 250 255  
 Cys Leu Phe Tyr Glu Val Glu Val Asn Asn Ser Gln Thr Glu Thr His  
 260 265 270  
 Asn Val Phe Tyr Val Gln Glu Ala Lys Cys Glu Asn Pro Glu Phe Glu  
 275 280 285  
 Arg Asn Val Glu Asn Thr Ser Cys Phe Met Val Pro Gly Val Leu Pro  
 290 295 300  
 Asp Thr Leu Asn Thr Val Arg Ile Arg Val Lys Thr Asn Lys Leu Cys  
 305 310 315 320  
 Tyr Glu Asp Asp Lys Leu Trp Ser Asn Trp Ser Gln Glu Met Ser Ile  
 325 330 335  
 Gly Lys Lys Arg Asn Ser Thr Leu Tyr Ile Thr Met Leu Leu Ile Val  
 340 345 350  
 Pro Val Ile Val Ala Gly Ala Ile Ile Val Leu Leu Leu Tyr Leu Lys  
 355 360 365  
 Arg Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile  
 370 375 380  
 Phe Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys  
 385 390 395 400  
 Lys Tyr Asp Ile Tyr Glu Lys Gln Thr Lys Glu Glu Thr Asp Ser Val  
 405 410 415  
 Val Leu Ile Glu Asn Leu Lys Lys Ala Ser Gln  
 420 425

<210> 5  
 <211> 420  
 <212> PRT  
 <213> Homo sapiens

<400> 5

Met Ile Ile Val Ala His Val Leu Leu Ile Leu Leu Gly Ala Thr Glu  
 1 5 10 15  
 Ile Leu Gln Ala Asp Leu Leu Pro Asp Glu Lys Ile Ser Leu Leu Pro  
 20 25 30  
 Pro Val Asn Phe Thr Ile Lys Val Thr Gly Leu Ala Gln Val Leu Leu  
 35 40 45  
 Gln Trp Lys Pro Asn Pro Asp Gln Glu Gln Arg Asn Val Asn Leu Glu  
 50 55 60  
 Tyr Gln Val Lys Ile Asn Ala Pro Lys Glu Asp Asp Tyr Glu Thr Arg  
 65 70 75 80  
 Ile Thr Glu Ser Lys Cys Val Thr Ile Leu His Lys Gly Phe Ser Ala  
 85 90 95  
 Ser Val Arg Thr Ile Leu Gln Asn Asp His Ser Leu Leu Ala Ser Ser  
 100 105 110  
 Trp Ala Ser Ala Glu Leu His Ala Pro Pro Gly Ser Pro Gly Thr Ser  
 115 120 125  
 Ile Val Asn Leu Thr Cys Thr Thr Asn Thr Thr Glu Asp Asn Tyr Ser  
 130 135 140  
 Arg Leu Arg Ser Tyr Gln Val Ser Leu His Cys Thr Trp Leu Val Gly  
 145 150 155 160  
 Thr Asp Ala Pro Glu Asp Thr Gln Tyr Phe Leu Tyr Tyr Arg Tyr Gly

31  
Cont

165 170 175  
 Ser Trp Thr Glu Glu Cys Gln Glu Tyr Ser Lys Asp Thr Leu Gly Arg  
 180 185 190  
 Asn Ile Ala Cys Trp Phe Pro Arg Thr Phe Ile Leu Ser Lys Gly Arg  
 195 200 205  
 Asp Trp Leu Ser Val Leu Val Asn Gly Ser Ser Lys His Ser Ala Ile  
 210 215 220  
 Arg Pro Phe Asp Gln Leu Phe Ala Leu His Ala Ile Asp Gln Ile Asn  
 225 230 235 240  
 Pro Pro Leu Asn Val Thr Ala Glu Ile Glu Gly Thr Arg Leu Ser Ile  
 245 250 255  
 Gln Trp Glu Lys Pro Val Ser Ala Phe Pro Ile His Cys Phe Asp Tyr  
 260 265 270  
 Glu Val Lys Ile His Asn Thr Arg Asn Gly Tyr Leu Gln Ile Glu Lys  
 275 280 285  
 Leu Met Thr Asn Ala Phe Ile Ser Ile Ile Asp Asp Leu Ser Lys Tyr  
 290 295 300  
 Asp Val Gln Val Arg Ala Ala Val Ser Ser Met Cys Arg Glu Ala Gly  
 305 310 315 320  
 Leu Trp Ser Glu Trp Ser Gln Pro Ile Tyr Val Gly Asn Asp Glu His  
 325 330 335  
 Lys Pro Leu Arg Glu Trp Phe Val Ile Val Ile Met Ala Thr Ile Cys  
 340 345 350  
  
 Phe Ile Leu Leu Ile Leu Ser Leu Ile Cys Lys Ile Cys His Leu Trp  
 355 360 365  
 Ile Lys Leu Phe Pro Pro Ile Pro Ala Pro Lys Ser Asn Ile Lys Asp  
 370 375 380  
 Leu Phe Val Thr Thr Asn Tyr Glu Lys Ala Gly Ser Ser Glu Thr Glu  
 385 390 395 400  
 Ile Glu Val Ile Cys Tyr Ile Glu Lys Pro Gly Val Glu Thr Leu Glu  
 405 410 415  
 Asp Ser Val Phe  
 420

<210> 6  
 <211> 424  
 <212> PRT  
 <213> Mus musculus

<400> 6

Met Ala Arg Pro Ala Leu Leu Gly Glu Leu Leu Val Leu Leu Leu Trp  
 1 5 10 15  
  
 Thr Ala Thr Val Gly Gln Val Ala Ala Ala Thr Glu Val Gln Pro Pro  
 20 25 30  
  
 Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Ile Ile Trp  
 35 40 45  
  
 Thr Trp Ser Pro Pro Glu Gly Ala Ser Pro Asn Cys Thr Leu Arg Tyr  
 50 55 60  
  
 Phe Ser His Phe Asp Asp Gln Gln Asp Lys Lys Ile Ala Pro Glu Thr  
 65 70 75 80  
  
 His Arg Lys Glu Glu Leu Pro Leu Asp Glu Lys Ile Cys Leu Gln Val  
 85 90 95

21  
 Cont

Gly Ser Gln Cys Ser Ala Asn Glu Ser Glu Lys Pro Ser Pro Leu Val  
 100 105 110  
 Lys Lys Cys Ile Ser Pro Pro Glu Gly Asp Arg Glu Ser Ala Val Thr  
 115 120 125  
 Glu Leu Lys Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser Trp  
 130 135 140  
 Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr His Tyr Thr Leu Tyr Tyr  
 145 150 155 160  
 Trp Tyr Ser Ser Leu Glu Lys Ser Arg Gln Cys Glu Asn Ile Tyr Arg  
 165 170 175  
 Glu Gly Gln His Ile Ala Cys Ser Phe Lys Leu Thr Lys Val Glu Pro  
 180 185 190  
 Ser Phe Glu His Gln Asn Val Gln Ile Met Val Lys Asp Asn Ala Gly  
 195 200 205  
 Lys Ile Arg Pro Ser Cys Lys Ile Val Ser Leu Thr Ser Tyr Val Lys  
 210 215 220  
 Pro Asp Pro Pro His Ile Lys His Leu Leu Leu Lys Asn Gly Ala Leu  
 225 230 235 240  
 Leu Val Gln Trp Lys Asn Pro Gln Asn Phe Arg Ser Arg Cys Leu Thr  
 245 250 255  
 Tyr Glu Val Glu Val Asn Asn Thr Gln Thr Asp Arg His Asn Ile Leu  
 260 265 270  
 Glu Val Glu Glu Asp Lys Cys Gln Asn Ser Glu Ser Asp Arg Asn Met  
 275 280 285  
 Glu Gly Thr Ser Cys Phe Gln Leu Pro Gly Val Leu Ala Asp Ala Val  
 290 295 300  
 Tyr Thr Val Arg Val Arg Val Lys Thr Asn Lys Leu Cys Phe Asp Asp  
 305 310 315 320  
 Asn Lys Leu Trp Ser Asp Trp Ser Glu Ala Gln Ser Ile Gly Lys Glu  
 325 330 335  
 Gln Asn Ser Thr Phe Tyr Thr Thr Met Leu Leu Thr Ile Pro Val Phe  
 340 345 350  
 Val Ala Val Ala Val Ile Ile Leu Leu Phe Tyr Leu Lys Arg Leu Lys  
 355 360 365  
 Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe Lys Glu  
 370 375 380  
 Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys Tyr Asp  
 385 390 395 400  
 Ile Tyr Glu Lys Gln Ser Lys Glu Glu Thr Asp Ser Val Val Leu Ile  
 405 410 415

31  
 Cont



Glu Asn Leu Lys Lys Ala Ala Pro  
420

<210> 7  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> primer

<400> 7

AGAGGAATTA CCCCTGGATG 20

<210> 8  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> anti-sense primer

<400> 8

TCAAGGAGCT GCTTTCTTCA 20

<210> 9  
<211> 21  
<212> DNA  
<213> Artificial sequence

<220>  
<223> primer

<400> 9

GATCCACTTC CCAAGAACAG A 21

<210> 10  
<211> 23  
<212> DNA  
<213> Artificial sequence

<220>  
<223> primer

<400> 10

GATCCGGGCC CTTTTTTTTT TTT 23

<210> 11  
<211> 6  
<212> PRT  
<213> Artificial sequence

31  
Cone

&lt;220&gt;

<223> in SEQ ID NO. 12, which is a variant of SEQ ID NO. 2, the sequence VRCVTL is substituted for the 8 C-terminal amino acids of the human protein.

&lt;400&gt; 11

Val Arg Cys Val Thr Leu  
1 5

&lt;210&gt; 12

&lt;211&gt; 378

&lt;212&gt; PRT

&lt;213&gt; Artificial sequence

&lt;220&gt;

<223> variant of SEQ ID NO. 2 in which the sequence VRCVTL is substituted for the 8 C-terminal amino acids of the human protein.

&lt;400&gt; 12

Met Ala Phe Val Cys Leu Ala Ile Gly Cys Leu Tyr Thr Phe Leu Ile  
1 5 10 15  
Ser Thr Thr Phe Gly Cys Thr Ser Ser Ser Asp Thr Glu Ile Lys Val  
20 25 30  
Asn Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr  
35 40 45  
Leu Tyr Leu Gln Trp Gln Pro Pro Leu Ser Leu Asp His Phe Lys Glu  
50 55 60  
Cys Thr Val Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Gly Ser Glu Thr  
65 70 75 80  
Trp Lys Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp  
85 90 95  
Leu Asn Lys Gly Ile Glu Ala Lys Ile His Thr Leu Leu Pro Trp Gln  
100 105 110  
Cys Thr Asn Gly Ser Glu Val Gln Ser Ser Trp Ala Glu Thr Thr Tyr  
115 120 125  
Trp Ile Ser Pro Gln Gly Ile Pro Glu Thr Lys Val Gln Asp Met Asp  
130 135 140  
Cys Val Tyr Tyr Asn Trp Gln Tyr Leu Leu Cys Ser Trp Lys Pro Gly  
145 150 155 160  
Ile Gly Val Leu Leu Asp Thr Asn Tyr Asn Leu Phe Tyr Trp Tyr Glu  
165 170 175  
Gly Leu Asp His Ala Leu Gln Cys Val Asp Tyr Ile Lys Ala Asp Gly  
180 185 190  
Gln Asn Ile Gly Cys Arg Phe Pro Tyr Leu Glu Ala Ser Asp Tyr Lys  
195 200 205  
  
Asp Phe Tyr Ile Cys Val Asn Gly Ser Ser Glu Asn Lys Pro Ile Arg  
210 215 220  
Ser Ser Tyr Phe Thr Phe Gln Leu Gln Asn Ile Val Lys Pro Leu Pro  
225 230 235 240  
Pro Val Tyr Leu Thr Phe Thr Arg Glu Ser Ser Cys Glu Ile Lys Leu  
245 250 255  
Lys Trp Ser Ile Pro Leu Gly Pro Ile Pro Ala Arg Cys Phe Asp Tyr  
260 265 270  
Glu Ile Glu Ile Arg Glu Asp Asp Thr Thr Leu Val Thr Ala Thr Val  
275 280 285  
Glu Asn Glu Thr Tyr Thr Leu Lys Thr Thr Asn Glu Thr Arg Gln Leu

21  
Cont

290		295		300
Cys Phe Val Val Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly				
305		310		315
Ile Trp Ser Glu Trp Ser Asp Lys Gln Cys Trp Glu Gly Glu Asp Leu				320
		325		330
Ser Lys Lys Thr Leu Leu Arg Phe Trp Leu Pro Phe Gly Phe Ile Leu				335
		340		345
Ile Leu Val Ile Phe Val Thr Gly Leu Leu Leu Arg Lys Pro Asn Thr				350
		355		360
Tyr Pro Lys Met Val Arg Cys Val Thr Leu				365
		370		375

<210> 13  
 <211> 5  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> motif characteristic of the family of chemokine receptors to which the polypeptides of SEQ ID NO. 2 and SEQ NO. 4 belong. Xaa can be any amino acid.

<400> 13

Trp Ser Xaa Trp Ser  
 1 5

<210> 14  
 <211> 6  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> polyadenylation signal

<400> 14

AATAAA 6

<210> 15  
 <211> 20  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> primer

<400> 15

AAAAAAAAAA AAAGGGCCCG 20

Fl  
Cont